



#8/A
PATENT
11/18/02

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In the Application of:

EDGAR B. CAHOON ET AL.

CASE NO.: BB1413 US NA

APPLN. NO.: 09/732,597

GROUP ART UNIT: 1638

FILED: DECEMBER 8, 2000

EXAMINER: E. F. MCELWAIN

FOR: ENZYMES INVOLVED IN PETROSELINIC
ACID BIOSYNTHESIS

RESPONSE TO RESTRICTION REQUIREMENT

RECEIVED

NOV 15 2002

Assistant Commissioner for Patents
Washington, DC 20231

TECH CENTER 1600/2900

Sir:

This is in response to the Office Action dated August 7, 2002 requiring restriction of claims 1-26. A Petition for Extension of Time for two (2) months up to and including November 7, 2002 is filed simultaneously herewith. The following is submitted in support thereof.

IN THE SPECIFICATION

Please amend the specification as follows; a marked-up version showing changes made is attached hereto:

Paragraph at page 10, lines 1-23:

A¹ A "substantial portion" of an amino acid or nucleotide sequence comprises an amino acid or a nucleotide sequence that is sufficient to afford putative identification of the protein or gene that the amino acid or nucleotide sequence comprises. Amino acid and nucleotide sequences can be evaluated either manually by one skilled in the art, or by using computer-based sequence comparison and identification tools that employ algorithms such as BLAST (Basic Local Alignment Search Tool; Altschul et al. (1993) *J. Mol. Biol.* 215:403-410). In general, a sequence of ten or more contiguous amino acids or thirty or more contiguous nucleotides is necessary in order to putatively identify a polypeptide or nucleic acid sequence as homologous to a known protein or gene. Moreover, with respect to nucleotide sequences, gene-specific oligonucleotide probes comprising 30 or more contiguous nucleotides may be used in sequence-dependent methods of gene identification (e.g., Southern hybridization) and isolation (e.g., *in situ* hybridization of bacterial colonies or bacteriophage plaques). In addition, short oligonucleotides of 12 or more nucleotides may be used as amplification primers in PCR in order to obtain a particular nucleic